

IntelliGenetics

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FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file seq72-t05430.res made by bobryen on Tue 17 Dec 102 12:59:17-PST.

Query sequence being compared: SEQ72-T05430 (1-217) 5
 Number of sequences searched: 5
 Number of scores above cutoff: 5

Results of the initial comparison of SEQ72-T05430 (1-217) with:
File : seq72compares.pep

[illegible]

PARAMETERS

	PAM-150	k-tuple
Similarity matrix		
Threshold level of sim.	16%	
Mismatch penalty	1	Joining penalty
Gap penalty	5.00	Window size
Gap size penalty	0.05	
Cutoff score	1	
Randomization group	0	

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	92	80	18.94
Times:	CPU	Total Elapsed	
	00:00:00.01	00:00:00.00	

Number of residues:	3817
Number of sequences searched:	5
Number of scores above cutoff:	5

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Score	Sig.	Frame
1. q9sr66	T22K18.18 protein.	1309	124	161	1.69	0
	*** 1 standard deviation above mean ***					
2. t48453	TOIG of t48453 check: 2431	555	95	104	0.16	0
3. q941x6	Putative FPPsynthasel (Fragme	119	84	94	-0.42	0
4. t05430	TOIG of: t05430 check: 9156	917	79	138	-0.69	0

1. SEQ72-T05430 (1-217)
q9sr66 T22K18.18 protein.

Initial Score	=	124	Optimized Score	=	161	Significance	=	1.69
Residue Identity	=	42%	Matches	=	93	Mismatches	=	86
Gaps	=	33	Conservative Substitutions	=	5			

[illegible]

2. ~~SEQ72-T05430 (1-217)~~
t48453 TOIG of: t48453 check: 2431 from: 1 to: 555

Initial Score	=	95	Optimized Score	=	104	Significance	=	0.16
Residue Identity	=	41%	Matches	=	60	Mismatches	=	74
Gaps	=	10	Conservative Substitutions	=	2		=	2

[illegible]

3. SEQ72-T05430 (1-217)
q94lx6 Putative FPP synthase1 (Fragment):

